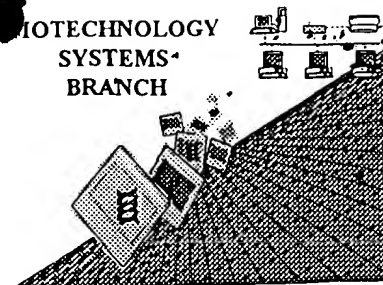


0590
0920

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 821 694
Source: OIPE
Date Processed by STIC: 09/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/821694

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/821,694

DATE: 09/18/2001

TIME: 11:23:44

Input Set : A:\0450001.app

Output Set: N:\CRF3\09182001\I821694.raw

3 <110> APPLICANT: HILLS, WILLIAM D.
 5 <120> TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
 6 HYBRIDIZATION
 8 <130> FILE REFERENCE: 0450-0001
 10 <140> CURRENT APPLICATION NUMBER: 09/821,694
 C--> 11 <141> CURRENT FILING DATE: 2001-08-31
 13 <160> NUMBER OF SEQ ID NOS: 50
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 13
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial Sequence ✓
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: Description of Artificial Sequence: Analyte ✓
 24 sequence
 26 <400> SEQUENCE: 1
 27 ataaagctgc ttc 13
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 23
 32 <212> TYPE: DNA ✓
 33 <213> ORGANISM: Artificial Sequence ✓
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: Description of Artificial Sequence: Labeling ✓
 37 structure
 39 <400> SEQUENCE: 2
 40 aaaaaaaaaac ccccttttct ttt 23
 43 <210> SEQ ID NO: 3
 44 <211> LENGTH: 23
 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: Description of Artificial Sequence: Labeling ✓
 50 structure
 52 <400> SEQUENCE: 3
 53 aaaaaaaaaac cccctttttt ttt 23
 56 <210> SEQ ID NO: 4
 57 <211> LENGTH: 23
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of Artificial Sequence: Labeling ✓
 63 structure
 65 <400> SEQUENCE: 4
 66 aaaagaaaac ccccttttct ttt 23
 69 <210> SEQ ID NO: 5
 70 <211> LENGTH: 14
 71 <212> TYPE: DNA

Does Not Comply
Corrected Diskette Needed

See page 3 of 7

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/821,694

TIME: 11:23:44

Input Set : A:\0450001.app

Output Set: N:\CRF3\09182001\I821694.raw

```

72 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
76     sequence
78 <400> SEQUENCE: 5
79 acgagctgcc agtc 14
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 14
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
89     sequence
91 <400> SEQUENCE: 6
92 gactggcagc tcga 14
95 <210> SEQ ID NO: 7
96 <211> LENGTH: 28
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
100 <220> FEATURE:
101 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
102     sequence
104 <220> FEATURE:
105 <221> NAME/KEY: modified_base
106 <222> LOCATION: (1)..(3)
107 <223> OTHER INFORMATION: a, t, g, or c
109 <220> FEATURE:
110 <221> NAME/KEY: modified_base ✓
111 <222> LOCATION: (4)
112 <223> OTHER INFORMATION: synthetic c or t nucleotide
114 <400> SEQUENCE: 7
W--> 115 nnnnmacgagc tgccagtcca tttaggcg 28
118 <210> SEQ ID NO: 8
119 <211> LENGTH: 28
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
125     sequence
127 <220> FEATURE:
128 <221> NAME/KEY: modified_base
129 <222> LOCATION: (1)..(3)
130 <223> OTHER INFORMATION: a, t, g, or c
132 <220> FEATURE:
133 <221> NAME/KEY: modified_base
134 <222> LOCATION: (4)
135 <223> OTHER INFORMATION: 8-oxo-dG
137 <400> SEQUENCE: 8
W--> 138 nnngacgagc tgccagtccg ctttgtag 28

```

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/821,694

TIME: 11:23:44

Input Set : A:\0450001.app

Output Set: N:\CRF3\09182001\I821694.raw

141 <210> SEQ ID NO: 9
 142 <211> LENGTH: 28
 143 <212> TYPE: DNA
 144 <213> ORGANISM: Artificial Sequence
 146 <220> FEATURE:
 147 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
 148 sequence
 150 <220> FEATURE:
 151 <221> NAME/KEY: modified_base
 152 <222> LOCATION: (1)..(2)
 153 <223> OTHER INFORMATION: a, t, g, or c
 155 <220> FEATURE:
 156 <221> NAME/KEY: modified_base
 157 <222> LOCATION: (2)
 158 <223> OTHER INFORMATION: synthetic c or t nucleotide
 160 <220> FEATURE:
 161 <221> NAME/KEY: modified_base
 162 <222> LOCATION: (3)
 163 <223> OTHER INFORMATION: a, t, g, or c
 165 <400> SEQUENCE: 9
 W--> 166 ~~nnn~~acgagc tgccagtcgg aacctgaa
 169 <210> SEQ ID NO: 10
 170 <211> LENGTH: 28
 171 <212> TYPE: DNA
 172 <213> ORGANISM: Artificial Sequence
 174 <220> FEATURE:
 175 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
 176 sequence
 178 <220> FEATURE:
 179 <221> NAME/KEY: modified_base
 180 <222> LOCATION: (1)..(2)
 181 <223> OTHER INFORMATION: a, t, g, or c
 183 <220> FEATURE:
 184 <221> NAME/KEY: modified_base
 185 <222> LOCATION: (3)
 186 <223> OTHER INFORMATION: 8-oxo-dG
 188 <220> FEATURE:
 189 <221> NAME/KEY: modified_base
 190 <222> LOCATION: (4)
 191 <223> OTHER INFORMATION: a, t, g or c
 193 <400> SEQUENCE: 10
 W--> 194 ~~nnn~~acgagc tgccagtcac tcctcctc 28
 197 <210> SEQ ID NO: 11
 198 <211> LENGTH: 28
 199 <212> TYPE: DNA
 200 <213> ORGANISM: Artificial Sequence
 202 <220> FEATURE:
 203 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
 204 sequence

Errors

Field 222 does not indicate an unknown at location four as indicated in the sequence listing.

may
The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/821,694

DATE: 09/18/2001
 TIME: 11:23:44

Input Set : A:\0450001.app
 Output Set: N:\CRF3\09182001\I821694.raw

```

206 <220> FEATURE:
207 <221> NAME/KEY: modified_base
208 <222> LOCATION: (1)
209 <223> OTHER INFORMATION: a, t, g, or c
211 <220> FEATURE:
212 <221> NAME/KEY: modified_base
213 <222> LOCATION: (2)
214 <223> OTHER INFORMATION: synthetic c or t nucleotide
216 <220> FEATURE:
217 <221> NAME/KEY: modified_base
218 <222> LOCATION: (3)..(4)
219 <223> OTHER INFORMATION: a, t, g, or c 0
221 <400> SEQUENCE: 11
W--> 222 nnnnacgagc tgccagtcgc aagaagtc 28
225 <210> SEQ ID NO: 12
226 <211> LENGTH: 28
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
232     sequence
234 <220> FEATURE:
235 <221> NAME/KEY: modified_base
236 <222> LOCATION: (1)
237 <223> OTHER INFORMATION: a, t, g, or c
239 <220> FEATURE:
240 <221> NAME/KEY: modified_base
241 <222> LOCATION: (2)
242 <223> OTHER INFORMATION: 8-oxo-dG
244 <220> FEATURE:
245 <221> NAME/KEY: modified_base
246 <222> LOCATION: (3)..(4)
247 <223> OTHER INFORMATION: a, t, g, or c
249 <400> SEQUENCE: 12
W--> 250 nnnnacgagc tgccagtcgc cgataact 28
253 <210> SEQ ID NO: 13
254 <211> LENGTH: 28
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
260     sequence
262 <220> FEATURE:
263 <221> NAME/KEY: modified_base
264 <222> LOCATION: (1)
265 <223> OTHER INFORMATION: synthetic c or t nucleotide
267 <220> FEATURE:
268 <221> NAME/KEY: modified_base
269 <222> LOCATION: (2)..(4)

```

RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/821,694

TIME: 11:23:44

Input Set : A:\0450001.app

Output Set: N:\CRF3\09182001\I821694.raw

```

270 <223> OTHER INFORMATION: a, t, g, or c
272 <400> SEQUENCE: 13
W--> 273 nnnnacgagc tgccagtcgc atccatct 28
276 <210> SEQ ID NO: 14
277 <211> LENGTH: 28
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
283     sequence
285 <220> FEATURE:
286 <221> NAME/KEY: modified_base
287 <222> LOCATION: (1)
288 <223> OTHER INFORMATION: 8-oxo-dG
290 <220> FEATURE:
291 <221> NAME/KEY: modified_base
292 <222> LOCATION: (2)..(4)
293 <223> OTHER INFORMATION: a, t, g, or c
295 <400> SEQUENCE: 14
W--> 296 nnnnacgagc tgccagtcgc cagtgtta 28
299 <210> SEQ ID NO: 15
300 <211> LENGTH: 28
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
306     sequence
308 <220> FEATURE:
309 <221> NAME/KEY: modified_base
310 <222> LOCATION: (1)..(3)
311 <223> OTHER INFORMATION: a, t, g, or c
313 <400> SEQUENCE: 15
W--> 314 nnnnyacgagc tgccagtcca tttaggcg 28
317 <210> SEQ ID NO: 16
318 <211> LENGTH: 28
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of Artificial Sequence: Adaptor ✓
324     sequence
326 <220> FEATURE:
327 <221> NAME/KEY: modified_base
328 <222> LOCATION: (1)..(3)
329 <223> OTHER INFORMATION: a, t, g, or c
331 <400> SEQUENCE: 16
W--> 332 nnnnkacgagc tgccagtccg ctttgtag 28
335 <210> SEQ ID NO: 17
336 <211> LENGTH: 28
337 <212> TYPE: DNA

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/821,694

DATE: 09/18/2001

TIME: 11:23:45

Input Set : A:\0450001.app

Output Set: N:\CRF3\09182001\I821694.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42